AMENDMENTS TO THE CLAIMS

1. (original) A method for identifying a non-uniform measured signal distribution in a region of a scanned image of a molecular array, the method comprising:

providing a variance model for measured signal distributions within regions of the molecular array;

determining a variance of measured signals within the region; and

determining whether or not the region contains a non-uniform measured signal distribution by comparing the determined variance of measured signals within the region to the variance model.

2. (original) The method of claim 1 further including determining a variance threshold from the variance model, and wherein comparing the determined variance of measured signals within the region to the variance model comprises comparing the determined variance of measured signals within the region to the determined variance threshold.

3. (original) The method of claim 2 wherein the scanned image comprises pixels, each pixel associated with a count representing a signal measured from a corresponding portion of the molecular array.

4. (original) The method of claim 3 wherein the variance model is a linear combination of model variance terms.

5. (currently amended) The method of claim 4 wherein model variance terms include:

a variance term arising from non-uniformities associated with target-molecule labeling, feature synthesis, probe molecule ~~application.~~ application, and other solution and surface chemistry effects;

a variance term arising from non-uniformities associated with scanner counting errors; and

a variance term arising from non-uniformities associated with electronic noise in a scanner, background-level signal noise arising from a molecular array substrate, and other noise.

6. (currently amended) The method of claim 5 wherein non-uniformities associated with target-molecule labeling, feature synthesis, probe molecule ~~application.~~ application, and other solution and surface chemistry effects are assumed to be normally distributed, wherein non-uniformities associated with scanner counting errors are modeled by a Poisson distribution, and wherein non-uniformities associated with electronic noise in the scanner, background-level signal noise produced by the molecular array substrate, and other noise are assumed to produce a constant variance.

7. (original) The method of claim 3 wherein the variance model is an expression including a mean pixel count for the region as a variable.

8. (currently amended) The method of claim 2 wherein calculating a variance threshold from the variance model further includes assuming a chi-squared distribution for one less than the number of pixels multiplied by the model variance and divided by the theoretical variance of measured signals within the region, and, based on the ~~chi0squared~~ chi-squared distribution assumption, selecting a threshold variance value below which the determined variance of measured signals within the region has a high probability of indicating an acceptably uniform distribution of measured signals within the region.

9. (original) The method of claim 1 wherein the region is selected from among a feature and a feature background.

10. (original) The method of claim 1 wherein the variance model is provided according to chemical and physical properties of the molecular array, electronic and physical properties of a scanning device, and experimental conditions to which the molecular array is exposed.

11. (original) A representation of a non-uniform measured signal distribution in a region of a scanned image of a molecular array identified by the method of claim 1 stored in a computer-readable medium.

12. (original) Results produced by a molecular array data processing program employing the method of claim 1 stored in a computer-readable medium.

13. (original) Results produced by a molecular array data processing program employing the method of claim 1 transferred to an intercommunicating entity via electronic signals.

14. (original) Results produced by a molecular array data processing program employing the method of claim 1 printed in a human-readable format.

15. (original) A system for identifying a non-uniform measured signal distribution in a region of a scanned image of a molecular array, the system comprising:

a digital representation of the measured signals in the region of the scanned image of the molecular array stored within a memory component;

a variance model for measured signal distributions within regions of the molecular array stored within a memory component; and

a computational processing engine that calculates a variance of measured signals within the region and compares the calculated variance with the variance model to determine whether or not the region contains a non-uniform measured signal distribution by comparing the determined variance of measured signals within the region to the variance model.

16. (original) The system of claim 15 wherein the variance model further includes a variance threshold to which the computational processing engine compares the calculated variance.

17. (original) The system of claim 15 wherein the digital representation of the measured signals in the region of the scanned image of the molecular array comprises a number of pixels, each pixel associated with a count representing a signal measured from a corresponding portion of the molecular array.

18. (original) The system of claim 15 wherein the variance model is a linear combination of model variance terms.

19. (currently amended) The system of claim 18 wherein model variance terms include:

a variance term arising from non-uniformities associated with target-molecule labeling, feature synthesis, probe molecule ~~application.~~ application, and other solution and surface chemistry effects;

a variance term arising from non-uniformities associated with scanner counting errors; and

a variance term arising from non-uniformities associated with electronic noise in a scanner, background-level signal noise arising from a molecular array substrate, and other noise.

20. (currently amended) The system of claim 19 wherein non-uniformities associated with target-molecule labeling, feature synthesis, probe molecule ~~application.~~ application, and other solution and surface chemistry effects are assumed to be normally distributed, wherein non-uniformities associated with scanner counting errors are modeled by a Poisson distribution, and wherein non-uniformities associated with electronic noise in the scanner, background-level signal noise produced by the molecular array substrate, and other noise are assumed to produce a constant variance.

21. (original) The system of claim 15 wherein the variance model is an expression including a mean pixel count for the region as a variable.

22. (original) The system of claim 15 wherein the variance model is based on chemical and physical properties of the molecular array, electronic and physical properties of a scanning device, and experimental conditions to which the molecular array is exposed.